

80837  
**Schreiber, David**

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**From:** Ramirez, Delia  
**Sent:** Thursday, November 21, 2002 11:59 AM  
**To:** Schreiber, David  
**Subject:** case 09/854844

Hi David,

I was wondering if you could do an alignment for me. It is seq id 1 against the DNA of accession XM\_093852 and seq id 2 against the protein encoded in XM\_093852, (LOC166414). Applicant's argue that this entry has 99% similarity to their seq id 2 but I could not find this in the first seach I did.

Thanks,

Delia

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(703) 306-0288  
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# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

## STAFF USE ONLY

Date completed: 11/21  
Searcher: D. Schreiber 308-492  
Terminal time: 42  
Elapsed time: 6  
CPU time: \_\_\_\_\_  
Total time: \_\_\_\_\_  
Number of Searches: \_\_\_\_\_  
Number of Databases: \_\_\_\_\_

Search Site  
\_\_\_\_ STIC  
☒ CM-1 6A03  
\_\_\_\_ Pre-S  
Type of Search  
☒ N.A. Sequence  
☒ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

Vendors  
\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
☒ Other compus  
www and 128

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|||||
Db 601 GAAGACAAGATTGTGCTGGTGATCTCAAAACATGAAGGATAGTTGCAAGGGTGATTCT 660
QY 661 GGAGGGCCTCTGCTGTCACATTGATGGTGTATGGATCCAGACAGGAGTAGTAAGCTGG 720
Db 661 GGAGGGCCTCTGCTGTCACATTGATGGTGTATGGATCCAGACAGGAGTAGTAAGCTGG 720
QY 721 GGATTAGAATGTGGTAAATCTCTTCTGGAGTCTACACCAATGTAATCTACTACCAAAAA 780
Db 721 GGATTAGAATGTGGTAAATCTCTTCTGGAGTCTACACCAATGTAATCTACTACCAAAAA 780
QY 781 TGGATTAAATGCCACTATTTCAGAGCCCAACAATCTAGACTTCTGACTTCTTGTTCCT 840
Db 781 TGGATTAAATGCCACTATTTCAGAGCCCAACAATCTAGACTTCTGACTTCTTGTTCCT 840
QY 841 ATTGTCTACTCTCTGGGCTCTCTGYGTCCCTCTGTCCTTGGACCTAAGACTATA 900
Db 841 ATTGTCTACTCTCTGGGCTCTCTGGGCTCTCTGGGCTCTCTGGGCTTGGACCTAAGACTATA 900
QY 901 CACAGAGTAGGCACCTGTAGCTGAAGCTGTGGCTTGCATACAGGGCTGGGAAGAGATGCA 960
Db 901 CACAGAGTAGGCACCTGTAGCTGAAGCTGTGGCTTGCATACAGGGCTGGGAAGAGATGCA 960
QY 961 TGGAGATTAGTCCAGGGGCAGAGAA 987
Db 961 TGGAGATTAGTCCAGGGGCAGAGAA 987

```

Search completed: November 21, 2002, 14:30:56  
Job time : 1 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model  
Run on: November 21, 2002, 14:34:26 ; Search time 0.001 Seconds  
(without alignments)  
113.488 Million cell updates/sec

Title: us-09-854-844-2  
Perfect score: 1863  
Sequence: 1 MGPAGCAFTLLLLGISVCG.....GRLTGEPLFLGDFIYNLK 346

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 328 residues

Total number of hits satisfying chosen parameters: 1

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 1 summaries

Database : loc166414.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1749	93.9	328	1 LOC166414	ACCESSION:XP_093855

ALIGNMENTS

RESULT 1  
LOC166414  
LOCUS LOC166414 328 aa linear PRI 13-MAY-2002  
DEFINITION similar to epidermis specific serine protease [Homo sapiens].  
ACCESSION XP\_093852  
VERSION XP\_093852.4 GI:20534016  
DBSOURCE REFSEQ: accession XM\_093852.4  
KEYWORDS  
SOURCE Homo sapiens  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
1 (residues 1 to 328)  
NCBI Annotation Project.  
Direct Submission  
Submitted (09-MAY-2002) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA  
GENOME ANNOTATION REFSEQ: This model reference sequence was predicted from NCBI contig NT\_022851 by automated computational analysis using gene prediction method: GenomeScan.  
Also see:  
Documentation of NCBI's Annotation Process

On May 13, 2002 this sequence version replaced gi:20503620.

FEATURES  
source Location/Qualifiers  
1..328  
/organism="Homo sapiens"

/db\_xref="taxon:9606"  
1..328  
/chromosome="4"  
/product="similar to epidermis specific serine protease"  
27..262  
/region\_name="Trypsin-like serine protease"  
/note="Tryp\_SPC"  
/db\_xref="CDD:smart00020"  
28..262  
/region\_name="Trypsin"  
/note="Trypsin"  
/db\_xref="CDD:pfam00089"  
1..328  
/gene="LOC166414"  
/coded\_by="XM\_093852.4:1..987"  
/db\_xref="InterimID:166414"

Query Match 93.9%; Score 1749; DB 1; Length 328;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 326; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MGPAGCAFTLLLLGISVCGQPVYSSRVVGGODAAAGRPWQVSLHFDHNFYGGSLVSE 60  
|||||

Db 1 MGPAGCAFTLLLLGISVCGQPVYSSRVVGGODAAAGRPWQVSLHFDHNFYGGSLVSE 60  
|||||

QY 61 RLILTAACHCIQPTWTFSTVVLGSIYVSGDSSRRKRVYVSKIVHPKYQDTTADVALLKL 120  
|||||

Db 61 RLILTAACHCIQPTWTFSTVVLGSIYVSGDSSRRKRVYVSKIVHPKYQDTTADVALLKL 120  
|||||

QY 121 SSQVTFSAIPLPSVTQKLAIPPCVWTGKVKESDRDYHSALQEAEPVPIIDROA 180  
|||||

Db 121 SSQVTFSAIPLPSVTQKLAIPPCVWTGKVKESDRDYHSALQEAEPVPIIDROA 180  
|||||

QY 181 CEQLYNPIGIFPALEPVIKEDKICAGDTQNMKDCCKGSGGSLCHIDGVWQTGVSW 240  
|||||

Db 181 CEQLYNPIGIFPALEPVIKEDKICAGDTQNMKDCCKGSGGSLCHIDGVWQTGVSW 240  
|||||

QY 241 GLECGKSLPGVYTNVIYQKWINATISRANNDLDFSLFPVILLSLALLCPSCAFGPNTI 300  
|||||

Db 241 GLECGKSLPGVYTNVIYQKWINATISRANNDLDFSLFPVILLSLALLCPSCAFGPNTI 300  
|||||

QY 301 HRVGTVAEAVACIQGWEENAWRFSPRGR 328  
|||||

Db 301 HRVGTVAEAVACIQGWEENAWRFSPRGR 328  
|||||

Search completed: November 21, 2002, 14:34:27

Job time : 1 secs

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